AMENDMENTS

Amendments to the claims:

Please amend claims 64, 65, 70, 71, as set forth in the complete listing of the claims that follows. This complete listing of the claims replaces previous claim listings.

1-63. (Cancelled)

64. (Currently amended) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set, the intermediate data set having a plurality of data values associated with respective points in an array of data;

compress the intermediate data set to obtain compressed data;

define putative peaks in the compressed ~~intermediate~~ data ~~set~~, wherein the putative peaks represent components in the DNA sample;

~~compress the intermediate data set to obtain compressed data;~~

generate a residual baseline by removing the putative peaks from the ~~intermediate~~ compressed data ~~set~~;

remove the residual baseline from the ~~intermediate~~ compressed data ~~set~~ to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein the compressed data comprise~~s~~ compressed data points and wherein a compressed data point is a real number that includes a whole number portion that is determined by calculating the difference between the whole number portions of ~~representing the difference between~~ two consecutive points in an array of data.

65. (Currently amended) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set, the intermediate data set having a plurality of data values associated with respective points in an array of data;

compress the intermediate data set to obtain compressed data;

define putative peaks in the compressed ~~intermediate~~ data ~~set~~, wherein the putative peaks represent components in the DNA sample;

~~compress the intermediate data set to obtain compressed data;~~

generate a residual baseline by removing the putative peaks from the ~~intermediate~~ compressed data ~~set~~;

remove the residual baseline from the ~~intermediate~~ compressed data ~~set~~ to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein the compressed data comprise~~s~~ compressed data points and wherein a compressed data point is a real number that includes a decimal portion representing the difference between a maximum value of all the data values and a value at a particular point in an array.

66-69. (Cancelled)

70. (Currently amended) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set, comprising the steps of

a) identifying the center line of each putative peak;

b) removing an area to the right of the center line of each putative peak; and

c) removing an area equal to twice the width of the Gaussian to the left of the center line of each putative peak;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak. ~~;~~

~~wherein generating the residual baseline includes deleting an area around each putative peak in the intermediate data set; the residual baseline is generated from data remaining in the intermediate data set after the areas around the putative peaks have been removed; and~~

~~wherein the area equal to twice the width of the Gaussian is removed from the left of the center line of each putative peak.~~

71. (Currently amended) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set, comprising the steps of

a) identifying the center line of each putative peak;

b) removing an area equal to the area corresponding to 50 Daltons along the x-axis to the right of the center line of each putative peak; and

c) removing an area to the left of the center line of each putative peak;

~~wherein generating the residual baseline includes deleting an area around each putative peak in the intermediate data set and the residual baseline is generated from data remaining in the intermediate data set after the areas around the putative peaks have been removed ;~~

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak. ~~;~~

~~wherein the area equivalent to 50 daltons is removed from the right of the center line of each putative peak.~~

72-78. (Cancelled)

79. (Previously presented) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein the identifying step includes determining a peak probability for the putative peak, and multiplying the peak probability by an allelic penalty to obtain a final peak probability.

80-81. (Cancelled)

82. (Previously presented) An automated method for identifying a component in a DNA sample, comprising:

using a mass spectrometer to generate a computer readable data set comprising data representing components in the biological sample for analysis by a computer, and using the computer to:

denoise the data set to generate denoised data;

correct a baseline from the denoised data to generate an intermediate data set;

define putative peaks in the intermediate data set, wherein the putative peaks represent components in the DNA sample;

generate a residual baseline by removing the putative peaks from the intermediate data set;

remove the residual baseline from the intermediate data set to generate a corrected data set;

locate a putative peak in the corrected data set; and

identify the component that corresponds to the located putative peak;

wherein the identifying step includes calculating a peak probability that a putative peak in the corrected data is a peak indicating composition of the DNA sample; and

wherein peak probability is calculated for each of a plurality of putative peaks in the corrected data and a highest probability is compared to a second-highest probability to generate a calling ratio.

83. (Previously presented) The method according to claim 82 wherein the calling ratio is used to determine if the composition of the DNA sample will be called.

84-91. (Cancelled)

92. (Previously presented) The method according to claim 79, wherein the peak probability is determined from a probability profile.

93. (Previously presented) The method according to claim 79, comprising determining an allelic ratio, wherein the allelic ratio is a comparison of two peak heights in the corrected data, and assigning the allelic penalty to the allelic ratio.